

M. Haddad



RAW SEQUENCE LISTING

DATE: 05/08/2002

PATENT APPLICATION: US/09/735,251

TIME: 11:23:02

Input Set : N:\Crf3\RULE60\09735251.raw

Output Set: N:\CRF3\05082002\I735251.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Reed, Guy

6 Clement, Christophe Y.

8 (ii) TITLE OF INVENTION: NOVEL PLATELET ACTIVATION PROTEIN

10 (iii) NUMBER OF SEQUENCES: 4

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Fish & Richardson P.C.

14 (B) STREET: 225 Franklin Street

15 (C) CITY: Boston

16 (D) STATE: MA

17 (E) COUNTRY: USA

18 (F) ZIP: 02110-2804

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette

22 (B) COMPUTER: IBM Compatible

23 (C) OPERATING SYSTEM: DOS

24 (D) SOFTWARE: FastSEQ Version 2.0

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/735,251

C--> 28 (B) FILING DATE: 12-Dec-2000

30 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/08/725,758A

33 (B) FILING DATE: 04-OCT-1996

35 (A) APPLICATION NUMBER: 60/005,074

36 (B) FILING DATE: 06-OCT-1995

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Fraser, Janis K.

40 (B) REGISTRATION NUMBER: 34,819

41 (C) REFERENCE/DOCKET NUMBER: 05433/020001

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 617-542-5070

45 (B) TELEFAX: 617-542-8906

46 (C) TELEX: 200154

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1373 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: both

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (ix) FEATURE:

60 (A) NAME/KEY: Coding Sequence

ENTERED

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61          (B) LOCATION: 44...1321
62          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63 GCGAGAGGGC CAGAGGAGAA AGAGAGAGCG CGAAAGAGAG AGG ATG TCT CTC TCA      55
64                                     Met Ser Leu Ser
65                                     1
66
67 GAC TGG CAC CTG GCG GTG AAG CTG GCT GAC CAG CCA CTT ACT CCA AAG      103
68 Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys
69      5      10      15      20
70 TCT ATT CTT CGG TTG CCA GAG ACA GAA CTG GGA GAA TAC TCG CTA GGG      151
71 Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly
72      25      30      35
73 GGC TAT AGT ATT TCA TTT CTG AAG CAG CTT ATT GCT GGC AAA CTC CAG      199
74 Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln
75      40      45      50
76 GAG TCT GTT CCA GAC CCT GAG CTG ATT GAT CTG ATC TAC TGT GGT CGG      247
77 Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg
78      55      60      65
79 AAG CTA AAA GAT GAC CAG ACA CTT GAC TTC TAT GGC ATT CAA CCT GGG      295
80 Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly
81      70      75      80
82 TCC ACT GTC CAT GTT CTG CGA AAG TCC TGG CCT GAA CCT GAT CAG AAA      343
83 Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys
84      85      90      95      100
85 CCG GAA CCT GTG GAC AAA GTG GCT GCC ATG AGA GAG TTC CGG GTG TTG      391
86 Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu
87      105      110      115
88 CAC ACT GCC CTG CAC AGC AGC TCC TCT TAC AGG GAG GCG GTC TTT AAG      439
89 His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys
90      120      125      130
91 ATG CTC AGC AAT AAG GAG TCT CTG GAT CAG ATC ATT GTG GCC ACC CCA      487
92 Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro
93      135      140      145
94 GGC CTC AGC AGT GAC CCT ATT GCT CTT GGG GTT CTC CAG GAC AAG GAC      535
95 Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp
96      150      155      160
97 CTC TTC TCT GTC TTC GCT GAT CCC AAT ATG CTT GAT ACG TTG GTG CCT      583
98 Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro
99      165      170      175      180
100 GCT CAC CCA GCC CTC GTC AAT GCC ATT GTC CTG GTT CTG CAC TCC GTA      631
101 Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val
102      185      190      195
103 GCA GGC AGT GCC CCA ATG CCT GGG ACT GAC TCC TCT TCC CGG AGC ATG      679
104 Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met
105      200      205      210
106 CCC TCC AGC TCA TAC CGG GAT ATG CCA GGT GGC TTC CTG TTT GAA GGG      727
107 Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly
108      215      220      225
109 CTC TCA GAT GAT GAG GAT GAC TTT CAC CCA AAC ACC AGG TCC ACA CCC      775
110 Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro

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127      230      235      240
129 TCT AGC AGT ACT CCC AGC TCC CGC CCA GCC TCC CTG GGG TAC AGT GGA      823
130 Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly
131 245      250      255      260
133 GCT GCT GGG CCC CGG CCC ATC ACC CAG AGT GAG CTG GCC ACC GCC TTG      871
134 Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu
135      265      270      275
137 GCC CTG GCC AGC ACT CCG GAG AGC AGC TCT CAC ACA CCG ACT CCT GGC      919
138 Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly
139      280      285      290
141 ACC CAG GGT CAT TCC TCA GGG ACC TCA CCA ATG TCC TCT GGT GTC CAG      967
142 Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln
143      295      300      305
145 TCA GGG ACG CCC ATC ACC AAT GAT CTC TTC AGC CAA GCC CTA CAG CAT      1015
146 Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His
147      310      315      320
149 GCC CTT CAG GCC TCT GGG CAG CCC AGC CTT CAG AGC CAG TGG CAG CCC      1063
150 Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro
151 325      330      335      340
153 CAG CTG CAG CAG CTA CGT GAC ATG GGC ATC CAG GAC GAT GAG CTG AGC      1111
154 Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser
155      345      350      355
157 CTG CGG CCC TGC AGG CCA CCG GTG GGG ACA TCC AAG CAG CCC TGG AGC      1159
158 Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys Gln Pro Trp Ser
159      360      365      370
161 TCA TCT TTG CTG GAG GAG CCC CAT GAA CTC CCT GCT TCC CCT GAA CCC      1207
162 Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala Ser Pro Glu Pro
163      375      380      385
165 CCA GCA AGT TGC AGA GGC TAC TGC CCT TGG GAG GCA CTC ATG AAG GTG      1255
166 Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala Leu Met Lys Val
167      390      395      400
169 CCT CCA TCT CTC CCT TCC CCA ATA TAC CTG ATG GTC AAC TCT AAA AAA      1303
170 Pro Pro Ser Leu Pro Ser Pro Ile Tyr Leu Met Val Asn Ser Lys Lys
171 405      410      415      420
173 AAA AAA AAA AAA AAA AAA TGAAATACCA CTACTCTGAT CGTTTTTTTCA CTGACCCG      1359
174 Lys Lys Lys Lys Lys Lys
175      425
177 GTGAGGCGGC GCGA      1373
180 (2) INFORMATION FOR SEQ ID NO: 2:
182 (i) SEQUENCE CHARACTERISTICS:
183 (A) LENGTH: 426 amino acids
184 (B) TYPE: amino acid
185 (D) TOPOLOGY: linear
187 (ii) MOLECULE TYPE: protein
189 (v) FRAGMENT TYPE: internal
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
193 Met Ser Leu Ser Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro
194 1 5 10 15
195 Leu Thr Pro Lys Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu

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196          20          25          30
197 Tyr Ser Leu Gly Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala
198          35          40          45
199 Gly Lys Leu Gln Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile
200          50          55          60
201 Tyr Cys Gly Arg Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly
202          65          70          75          80
203 Ile Gln Pro Gly Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu
204          85          90          95
205 Pro Asp Gln Lys Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu
206          100          105          110
207 Phe Arg Val Leu His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu
208          115          120          125
209 Ala Val Phe Lys Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile
210          130          135          140
211 Val Ala Thr Pro Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu
212          145          150          155          160
213 Gln Asp Lys Asp Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp
214          165          170          175
215 Thr Leu Val Pro Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val
216          180          185          190
217 Leu His Ser Val Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser
218          195          200          205
219 Ser Arg Ser Met Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe
220          210          215          220
221 Leu Phe Glu Gly Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr
222          225          230          235          240
223 Arg Ser Thr Pro Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu
224          245          250          255
225 Gly Tyr Ser Gly Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu
226          260          265          270
227 Ala Thr Ala Leu Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr
228          275          280          285
229 Pro Thr Pro Gly Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser
230          290          295          300
231 Ser Gly Val Gln Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln
232          305          310          315          320
233 Ala Leu Gln His Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser
234          325          330          335
235 Gln Trp Gln Pro Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp
236          340          345          350
237 Asp Glu Leu Ser Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys
238          355          360          365
239 Gln Pro Trp Ser Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala
240          370          375          380
241 Ser Pro Glu Pro Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala
242          385          390          395          400
243 Leu Met Lys Val Pro Pro Ser Leu Pro Ser Pro Ile Tyr Leu Met Val
244          405          410          415

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245 Asn Ser Lys Lys Lys Lys Lys Lys Lys Lys
246           420           425
249 (2) INFORMATION FOR SEQ ID NO: 3:
251   (i) SEQUENCE CHARACTERISTICS:
252       (A) LENGTH: 1273 base pairs
253       (B) TYPE: nucleic acid
254       (C) STRANDEDNESS: both
255       (D) TOPOLOGY: linear
257   (ii) MOLECULE TYPE: cDNA
259   (ix) FEATURE:
260       (A) NAME/KEY: Coding Sequence
261       (B) LOCATION: 44...1273
263   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
265 GCGAGAGGGC CAGAGGAGAA AGAGAGAGCG CGAAAGAGAG AGG ATG TCT CTC TCA      55
266                               Met Ser Leu Ser
267                               1
269 GAC TGG CAC CTG GCG GTG AAG CTG GCT GAC CAG CCA CTT ACT CCA AAG      103
270 Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys
271   5           10           15           20
273 TCT ATT CTT CGG TTG CCA GAG ACA GAA CTG GGA GAA TAC TCG CTA GGG      151
274 Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly
275           25           30           35
277 GGC TAT AGT ATT TCA TTT CTG AAG CAG CTT ATT GCT GGC AAA CTC CAG      199
278 Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln
279           40           45           50
281 GAG TCT GTT CCA GAC CCT GAG CTG ATT GAT CTG ATC TAC TGT GGT CGG      247
282 Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg
283           55           60           65
285 AAG CTA AAA GAT GAC CAG ACA CTT GAC TTC TAT GGC ATT CAA CCT GGG      295
286 Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly
287           70           75           80
289 TCC ACT GTC CAT GTT CTG CGA AAG TCC TGG CCT GAA CCT GAT CAG AAA      343
290 Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys
291           85           90           95           100
293 CCG GAA CCT GTG GAC AAA GTG GCT GCC ATG AGA GAG TTC CGG GTG TTG      391
294 Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu
295           105           110           115
297 CAC ACT GCC CTG CAC AGC AGC TCC TCT TAC AGG GAG GCG GTC TTT AAG      439
298 His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys
299           120           125           130
301 ATG CTC AGC AAT AAG GAG TCT CTG GAT CAG ATC ATT GTG GCC ACC CCA      487
302 Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro
303           135           140           145
305 GGC CTC AGC AGT GAC CCT ATT GCT CTT GGG GTT CTC CAG GAC AAG GAC      535
306 Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp
307           150           155           160
309 CTC TTC TCT GTC TTC GCT GAT CCC AAT ATG CTT GAT ACG TTG GTG CCT      583
310 Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro
311 165           170           175           180

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VERIFICATION SUMMARY

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DATE: 05/08/2002

TIME: 11:23:03

Input Set : N:\Crf3\RULE60\09735251.raw

Output Set: N:\CRF3\05082002\I735251.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]